Geometric and Phenomenological Representation of the Genetic Code: A 3D Convex Hull Approach

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The genetic code, traditionally represented in linear or tabular formats, dictates the synthesis of proteins crucial to cellular functions across all life forms. However, these representations do not capture the spatial complexities and interactional dynamics inherent in genetic coding. Our study introduces a novel approach by mapping the genetic code onto a three-dimensional space, utilizing the mathematical construct of a 3D convex hull. This model not only visualizes the genetic code in an innovative manner but also enhances understanding of its structural and functional intricacies. By representing the centers of mass for amino acids within a polyhedral structure, we provide a fresh perspective on the relationships and evolutionary pathways encoded within this fundamental biological system. This approach bridges the fields of mathematics, biology, and phenomenology, offering a comprehensive framework to explore the genetic code's architecture and its implications on our understanding of life.

Keywords: genetic code, 3D convex hull, amino acids, codon mapping, mathematical biology, protein synthesis, evolutionary biology, phenomenology, geometric modeling, bioinformatics.

Abstract

In this study, we employ a geometric approach to visualize the genetic code through the construction of a 3D convex hull, representing the centers of mass for amino acids encoded by nucleotide triplets—codons. This model transcends traditional linear and planar representations by situating the genetic code within a three-dimensional space that reflects the physicochemical properties and relationships inherent in the molecular structure of life's fundamental building blocks. Our methodology involves mapping the codons to a three-dimensional grid based on nucleotide positions, thereby creating a spatial representation that encapsulates the coding potential of RNA sequences. Through the application of convex hull calculations, we delineate the bounds of this codonic space, offering a new lens through which to understand the encoding capacity of the genetic language.

The findings reveal a polyhedral framework in which each face corresponds to a specific combination of amino acids, with the overall shape encapsulating the diversity and redundancy of the genetic code. This representation not only contributes to a deeper mathematical appreciation of the genetic code's structure but also provokes a phenomenological discourse on the nature of genetic information encoding. By presenting the genetic code within the realm of geometric structures, we invite a fusion of mathematical rigor and philosophical inquiry, providing a fresh perspective on the interplay between the abstract constructs of human cognition and the tangible mechanisms of biological systems.

Introduction

The genetic code serves as the quintessential blueprint of life, directing the synthesis of proteins that are vital for cellular function. Traditionally, the code is delineated as a table correlating nucleotide triplets, or codons, with their corresponding amino acids. This linear representation, while

foundational, offers limited insights into the spatial and interactional nuances that characterize protein synthesis.

Our study aims to deepen the understanding of the genetic code by transposing it from a two-dimensional array into a three-dimensional structure, providing a novel perspective on the intrinsic patterns and redundancies present within this complex biological system. By utilizing the principles of convex geometry, we construct a 3D convex hull that spatially embodies the centers of mass for amino acids as dictated by their respective codons. This geometrical construct not only illustrates the physical space encompassed by the genetic code but also serves as a metaphor for the conceptual territory it occupies.

The 3D convex hull is a mathematical construct that encapsulates the smallest convex set containing a given set of points. In the context of the genetic code, these points correspond to the weighted average positions of codons for each amino acid, offering a visual and quantitative means to explore the distribution and relationships between them. The convex hull thus provides an interpretive framework, allowing for a more dynamic understanding of the genetic code's architecture. The relevance of this approach is twofold: it enhances our grasp of molecular biology's fundamental principles and enriches the phenomenological discourse on the way information is shaped and perceived in biological entities.

This innovative representation not only contributes to the scientific examination of genetic patterns but also invites reflection on the broader implications of understanding life's underpinnings through a geometric lens. As we embark on this interdisciplinary journey, the study stands as a testament to the synergy between mathematics, biology, and philosophy, and underscores the potential of such collaborations in unveiling the deeper workings of natural phenomena.

Methodology

The cornerstone of our methodology lies in the genetic code mapping— a comprehensive dataset that matches the 64 possible codons to their corresponding amino acids, including the designated stop signals which terminate translation. This dataset encapsulates the universal language through which genetic information is transcribed and translated, forming a foundational basis for protein synthesis across all forms of life.

Our computational approach begins with the translation of this genetic dataset into a three-dimensional Cartesian coordinate system, with each nucleotide within a codon assigned a specific numerical value that corresponds to a position along an axis. By assigning the nucleotide bases adenine (A), cytosine (C), guanine (G), and uracil (U) incrementally positioned values, we establish a spatial grid in which each codon can be placed based on its nucleotide sequence. This process transforms the abstract sequence data into a tangible point cloud within a cubic space, where each point is a representation of a codon, and thus, by proxy, the amino acid it encodes.

The mathematical concept of the center of mass plays a pivotal role in our analysis. For each amino acid, the center of mass is calculated as the mean position of all its codons' coordinates. This averaging process effectively consolidates the multiplicity of codons for each amino acid into a singular, representative point, encapsulating the distribution of its coding sequences within the three-dimensional space.

Upon establishing these centers, we apply the mathematical algorithm of the convex hull. The convex hull is the smallest convex shape that encompasses all points within a dataset. In a three-dimensional context, this shape is a polyhedron made up of vertices (the amino acid centers), edges, and faces. We compute the convex hull to provide not only a boundary to the codonic space but also to illustrate the relational structure between the different amino acids as determined by the genetic code.

To further enhance our analysis, we explore the concept of degeneracy— the redundancy of the genetic code wherein multiple codons encode for a single amino acid. The degeneracy is quantitatively assessed and mapped onto the constructed polyhedron, assigning a degeneracy value to each face based on the vertices that define it. This step melds the geometric representation with the functional characteristic of the genetic code, offering a multi-dimensional narrative of genetic encoding.

By leveraging a combination of Python programming and mathematical libraries, we computationally render the 3D convex hull, facilitating a visual and analytical exploration of the genetic code. This computational methodology not only underscores the genetic code's inherent complexity but also unveils patterns and relationships that are obscured in conventional linear representations.

Mathematical Model of Codon Space

The mathematical model of codon space is predicated upon a framework where the abstract sequences of nucleotides are translated into a quantifiable three-dimensional realm. This translation necessitates a systematic approach to nucleotide position mapping— a method that assigns a distinct, numerical value to each of the four nucleotide bases. The conventional genetic code table is reimagined as a three-dimensional grid where each axis corresponds to a position within a codon: the first, second, and third nucleotide positions. The nucleotides guanine (G), adenine (A), cytosine (C), and uracil (U) are mapped to positions with values 0, 0.333, 0.667, and 1.0, respectively, reflecting a normalized range that spans from 0 to 1. This specific mapping maintains the equidistant separation of nucleotide positions while anchoring the sequence space within a unit cube.

The codon, a triplet of nucleotides, thereby transforms into a point in 3D space, with its coordinates determined by the aforementioned positional

values. For instance, the codon AUG, which codes for the amino acid methionine, is assigned coordinates (0.333, 1.0, 0.333) corresponding to the A (adenine), U (uracil), and G (guanine) positions. This mapping transcribes the entire genetic code into a discrete set of points within the unit cube, with each point's location being a reflection of its constituent nucleotides.

Derivation of the amino acid centers of mass follows from this positional mapping. Each amino acid is encoded by a set of codons, ranging from a singular codon to as many as six. The center of mass for each amino acid is determined by taking the arithmetic mean of the coordinates of its codons. This mean represents the centroid of the points within the 3D space and is indicative of the average position of the amino acid's codons in the genetic landscape. Mathematically, the center of mass $\mathbf{c}_{\mathrm{a}}$ for amino acid a encoded by codons $\mathbf{c}_1,\mathbf{c}_2,\ldots,\mathbf{c}_n$ is calculated as:

where n is the number of codons that encode for the amino acid a, and $\mathbf{c}_i$ is the 3D coordinate of the ith codon.

$$\mathbf{c}_{\mathrm{aa}} = \frac{1}{n}\sum_{i=1}^{n}\mathbf{c}_i$$

where n is the number of codons that encode for the amino acid a, and $\mathbf{c}_i$ is the 3D coordinate of the ith codon.

The result is a distinct point for each of the 20 standard amino acids and the stop signal in the genetic code, each point a weighted locus of its genetic encoding. It is from these points that the model of codon space emerges as a constellation of centers, the precursors to the convex hull construction. This center of mass aggregation embodies a confluence of genetic variety and redundancy, providing the foundation for the subsequent geometric construction that encapsulates the comprehensive genetic code within a singular, unifying structure.

Construction of the 3D Convex Hull

The construction of the 3D convex hull is a process that seeks to envelop the set of points representing the centers of mass for amino acids within the smallest possible convex boundary. In the context of our model, each point corresponds to the centroid of an amino acid's codon coordinates, and the hull encloses the entirety of this biological dataset within a polyhedral shape. This construction is achieved computationally through an algorithmic approach that iterates over the points to identify the outermost vertices that form the convex boundary.

The computation process of the convex hull can be envisioned as the three-dimensional equivalent of stretching an elastic membrane around a set of objects, such that it snugly encases all objects and snaps back to the outermost points. Algorithmically, this is often executed using techniques such as the Quickhull algorithm, which functions by recursively determining the external faces of the hull. Starting with an initial simplex that is assured to be part of the convex hull, the algorithm finds the furthest point from each face of the simplex and creates new faces between this point and the edges of the original face. This process continues, with points inside the hull being ignored, until no points are left outside the hull.

The mathematical significance of constructing a convex hull in our context lies in its ability to translate the abstract, high-dimensional space of genetic sequences into a tangible geometric shape that can be analyzed and visualized. The convex hull serves not merely as a boundary but as a conceptual framework that simplifies complex relationships into a form amenable to geometric and topological analysis. The resulting polyhedron reveals the outermost limits of genetic variability and redundancy, providing a clear visual metaphor for the scope and structure of the genetic code.

By encapsulating the centers of mass within this convex boundary, the hull essentially maps out the 'shape' of the genetic code. It highlights the maximal dispersion of codons for each amino acid while also identifying the

collective proximity between different amino acid groups. This geometric perspective reveals the multidimensional nature of the genetic code, illustrating the volumetric space within which genetic evolution and molecular diversity operate.

Moreover, the construction of the convex hull has implications for understanding the underlying principles of the genetic code's organization. It allows for the identification of the most 'extreme' points—those amino acids whose codon sequences occupy unique positions in the codon space. This can shed light on the underlying symmetry or asymmetry in the genetic code and may have implications for understanding the physicochemical constraints that have shaped its evolution.

In essence, the convex hull provides a scaffolding to understand not just the individual coding sequences but also the collective interaction and arrangement of all coding sequences as a whole. It serves as a bridge between the abstract world of genetic information and the concrete realm of spatial geometry, fostering an understanding of the genetic code that is at once rigorous and intuitive.

Phenomenological Aspects

In the phenomenological exploration of the genetic code through the 3D convex hull, we transcend beyond the purely mathematical model to interpret the genetic structure through the lens of human experience and consciousness. The convex hull, as a phenomenological model, becomes not just a spatial object but also a symbolic representation of the ways in which we comprehend and interact with the abstract notion of genetic information. It embodies the inherent redundancies and efficiencies in the system, reflecting both the material reality of molecular biology and the conceptual frameworks that guide our understanding of it.

Codon degeneracy, the characteristic of the genetic code whereby multiple codons correspond to a single amino acid, is inherently tied to the evolutionary robustness of biological systems, safeguarding against mutations. Within the 3D convex hull, degeneracy is visualized through the multidimensional connections between points: the edges and faces of the hull represent the potential for codons to interchange without altering the amino acid they encode, and thus, the phenotype. In the phenomenological sense, the concept of degeneracy within this polyhedral form encapsulates the resilience and adaptability of life.

The phenomenological interpretation of this model lies in its ability to make tangible the abstractions of genetic coding. The geometric representation invites us to consider how the intricacies of the code relate to the lived experiences of organisms, including the constraints and possibilities embedded within the genetic language. The convex hull model thus serves as a bridge between the empirical reality of genetic coding and the ways in which such coding manifests in the observable traits and behaviors of organisms.

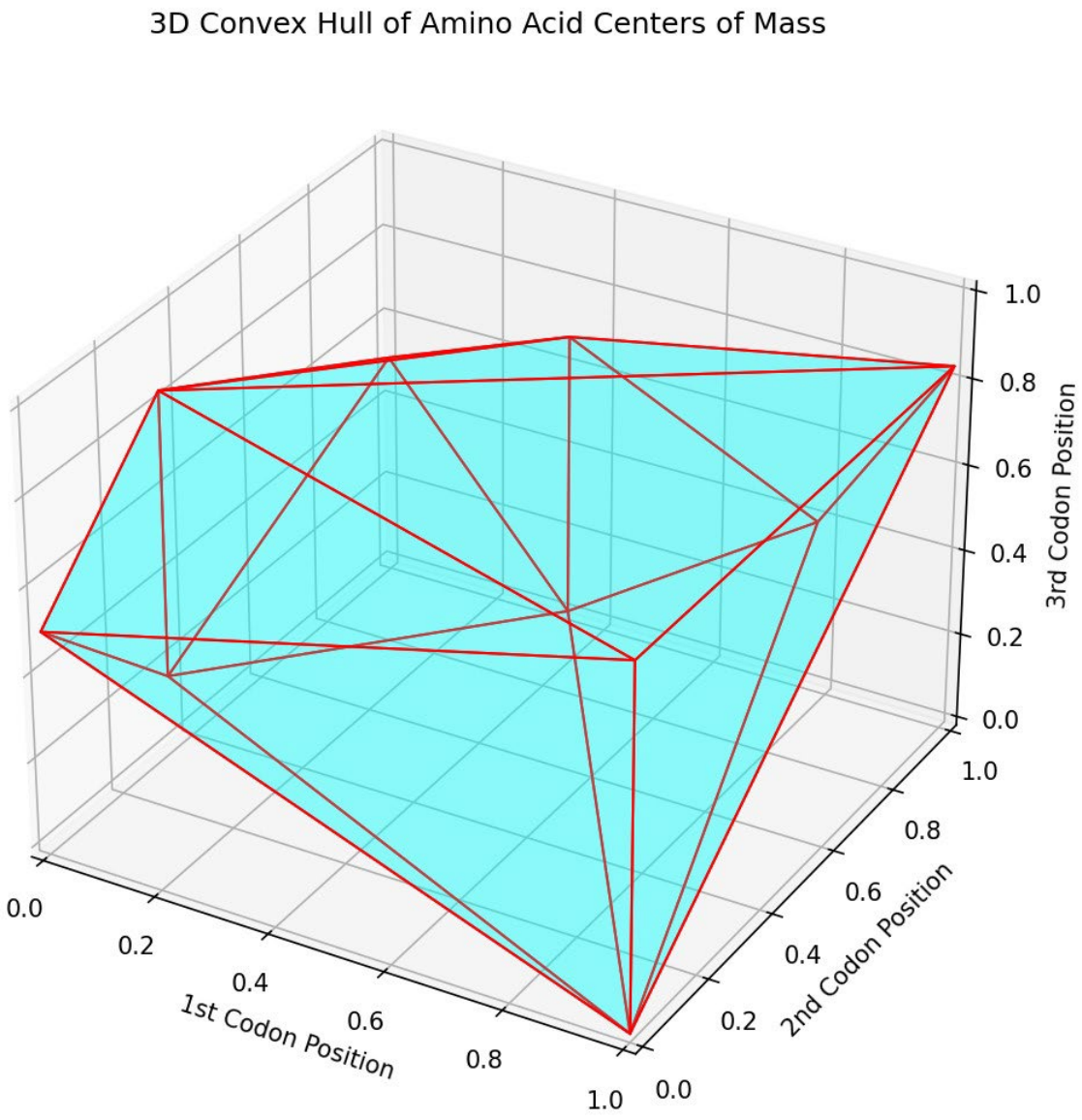
Furthermore, the representation of the genetic code as a 3D convex hull allows for a contemplation of the ways in which life's diversity can be understood as variations within a defined space. The faces of the hull, each corresponding to a specific amino acid combination, serve as a metaphor for the multitude of life forms and biological functions that arise from a finite set of genetic instructions. In this manner, the model elevates the genetic code from a fixed catalog of instructions to a dynamic field of potential, inviting deeper inquiry into the nature of biological information as it is expressed through the physical form.

By engaging with the genetic code through this phenomenological approach, we not only gain insights into the structural properties of the code but also grapple with the essence of what it means to encode life itself. This perspective illuminates the interplay between chance and necessity, randomness and order, highlighting the dialectical process by which life evolves and adapts. The 3D convex hull becomes more than a

mathematical construct; it becomes a narrative device, weaving the story of life's complexity and the resilience encapsulated within the genetic lexicon.

Results

In presenting the results of our study, the 3D convex hull visualization stands as the centerpiece, revealing a geometric embodiment of the genetic code's complexity. The visualization captures the centers of mass for the amino acids, depicted as nodes within a three-dimensional lattice. These nodes are interconnected, forming a polyhedral shape that is both aesthetically engaging and informatively rich. Each vertex represents the average position of a particular amino acid's codons within the genetic space, and each edge denotes a potential mutational path between amino acids within the code. The transparent faces, meanwhile, serve to demarcate boundaries between the functional groupings of these genetic instructions.



This graphical representation allows us to observe the relative positioning of amino acids in genetic space, offering insights into their interaction and evolutionary significance. For example, amino acids with a larger number of codons occupy a more central position within the hull, indicative of their foundational role in protein synthesis. Conversely, those encoded by fewer codons are found toward the hull's vertices, suggesting a specialized, perhaps more recent, evolutionary development.

The convex hull computation provides a structural map of the genetic code, showcasing the direct relationship between the geometry of the space and the biological phenomenon of protein encoding. This representation highlights areas of high and low codon degeneracy, which are of particular interest. Faces of the convex hull with greater surface areas correlate with higher degeneracy, indicating a robust buffer against mutations, as multiple codons can mutate without altering the resulting amino acid, and thus the structure of the protein.

The degeneracy analysis further elaborates on this concept. By examining the faces of the polyhedron, we uncover the collective degeneracy that characterizes the structure and function of proteins. Each face's degeneracy reflects the evolutionary pressures that have shaped the genetic code, suggesting that areas of greater degeneracy may correspond to regions of the protein that are more tolerant to mutations.

```
Microsoft Windows [Version 10.0.22631.3447]
(c) Microsoft Corporation. All rights reserved.

C:\Users\doug>python hull5.py
Degeneracy for each face:
Face defined by vertices ['W', 'G', 'C']: Total Degeneracy = 7
Face defined by vertices ['W', 'L', 'M']: Total Degeneracy = 8
Face defined by vertices ['W', 'C', 'F']: Total Degeneracy = 5
Face defined by vertices ['W', 'L', 'F']: Total Degeneracy = 9
Face defined by vertices ['D', 'C', 'F']: Total Degeneracy = 6
Face defined by vertices ['D', 'G', 'C']: Total Degeneracy = 8
Face defined by vertices ['E', 'W', 'M']: Total Degeneracy = 4
Face defined by vertices ['E', 'W', 'G']: Total Degeneracy = 7
Face defined by vertices ['E', 'M', 'V']: Total Degeneracy = 7
Face defined by vertices ['I', 'D', 'V']: Total Degeneracy = 9
Face defined by vertices ['I', 'D', 'F']: Total Degeneracy = 7
Face defined by vertices ['E', 'D', 'G']: Total Degeneracy = 8
Face defined by vertices ['E', 'D', 'V']: Total Degeneracy = 8
Face defined by vertices ['I', 'L', 'F']: Total Degeneracy = 11
Face defined by vertices ['I', 'M', 'V']: Total Degeneracy = 8
Face defined by vertices ['I', 'L', 'M']: Total Degeneracy = 10
```

Through this analysis, the 3D convex hull serves not only as a static model but as a dynamic framework within which the processes of genetic variation and protein synthesis can be explored. The visualization and the associated degeneracy analysis elucidate the underlying principles of the genetic code in a way that is both comprehensible and visually intuitive, offering a new method to examine the interdependence of structure and function within the context of genetic information encoding.

Discussion

The 3D convex hull model elucidates the genetic code in a manner that traditional two-dimensional representations cannot. Where a 2D model conveys information linearly or in a tabular form, the 3D convex hull encapsulates the volumetric aspect of genetic information, providing a more nuanced appreciation of the interrelations and distances between the codons and the amino acids they encode. This spatial model accentuates the dense and sparse regions of the genetic code, highlighting the intricate balance between genetic variability and conservation.

By interpreting the genetic code through the 3D convex hull, we gain a vantage point that reveals the multi-dimensional nature of genetic coding and expression. This model allows us to perceive the genetic code as a dynamic entity, wherein the spatial proximities of amino acid centroids suggest potential pathways for evolutionary transitions. Amino acids with codons closely clustered in space may reveal evolutionary and functional relationships that are obscured in flat representations. Conversely, the spatial segregation of certain amino acid centroids may indicate a higher selective pressure against substitution, potentially correlated with critical roles in protein structure and function.

The comparison with 2D models is significant. While 2D models of the genetic code are useful for straightforward tasks such as decoding or identifying mutations, they lack the capacity to depict the depth of

interactions and the three-dimensional constraints imposed by molecular structures. The 3D convex hull model transcends this limitation, providing a volumetric perspective that can more accurately mirror the complexity of molecular biology and the nuances of protein synthesis.

Phenomenologically, the model invites us to reconsider our conceptualization of the genetic code. No longer a static map of life's possibilities, the genetic code is now presented as a dynamic space ripe with potential for change and adaptation. The model becomes a narrative device, telling the story of genetic diversity and the evolutionary tale of life on Earth through its geometry. The spatial relationships within the convex hull shape our understanding of biological processes, echoing the very essence of phenomenology by bridging the gap between empirical observation and the human experience of understanding.

Furthermore, the 3D convex hull model provides a concrete form to the abstract concept of genetic information, offering a tool through which to visually and conceptually grasp the intricacies of molecular genetics. This geometrical interpretation of the genetic code could serve as a pedagogical aid, a research tool, and a theoretical framework, potentially influencing the way biological data is modeled, interpreted, and understood.

In the discussion of the model's implications, we must acknowledge that while the convex hull offers a new perspective, it is a simplification. The true behavior of genetic material is influenced by a myriad of factors beyond spatial coding—including regulatory elements, epigenetic modifications, and environmental interactions. The model, therefore, is not an endpoint but a starting point for further investigation and contemplation of the living language that is the genetic code.

Conclusion

In this study, we have extended the representation of the genetic code beyond traditional linear and tabular models by constructing a 3D convex hull that spatially embodies the centers of mass for amino acids as determined by their corresponding codons. This approach has unveiled a comprehensive visual and geometric representation of the genetic code, highlighting the structural nuances and potential evolutionary pathways within a polyhedral framework.

Key findings from our work demonstrate that the genetic code can be effectively modeled in three dimensions, where each amino acid's position is defined by the collective centroid of its codons. The 3D convex hull constructed from these points encapsulates the entire genetic code within the smallest possible convex volume, offering a novel perspective on the relationships between different amino acids. The visualization of this model has revealed the dense clustering of certain amino acids and the relative isolation of others, providing insights into the evolutionary pressures and functional constraints that shape the genetic landscape.

The analysis of codon degeneracy within this geometric framework has further enriched our understanding, illustrating how the redundancy built into the genetic code can be interpreted as a form of evolutionary resilience. Faces of the convex hull with higher degeneracy indicate regions of the genetic code that are robust to mutations, highlighting the adaptive strategies of biological systems at the molecular level.

Reflecting on the interplay between mathematics, biology, and phenomenology, this study exemplifies how mathematical concepts and techniques can provide profound insights into biological phenomena. The convex hull serves not only as a mathematical construct but also as a phenomenological model that invites deeper exploration into how genetic information is both structured and perceived. This blending of disciplines enhances our understanding of the genetic code not just as a series of

chemical instructions but as a dynamic system full of potential and variability.

This interdisciplinary approach underscores the importance of integrating mathematical rigor with biological inquiry to foster a more holistic understanding of life's complexities. By viewing the genetic code through both empirical and phenomenological lenses, we open new avenues for scientific exploration and philosophical reflection, challenging existing paradigms and encouraging a more nuanced appreciation of the underlying principles that govern biological information. The study not only contributes to our scientific knowledge but also enriches the broader discourse on the nature of life and the myriad ways we come to understand and represent it.

Python Code

```
import numpy as np
import matplotlib.pyplot as plt
from mpl_toolkits.mplot3d import Axes3D
from scipy.spatial import ConvexHull
from mpl_toolkits.mplot3d.art3d import Poly3DCollection

# Genetic code mapping from codons to single-letter amino acids
genetic_code = {
    'UUU': 'F', 'UUC': 'F', 'UUA': 'L', 'UUG': 'L',
    'CUU': 'L', 'CUC': 'L', 'CUA': 'L', 'CUG': 'L',
    'AUU': 'I', 'AUC': 'I', 'AUA': 'I', 'AUG': 'M',
    'GUU': 'V', 'GUC': 'V', 'GUA': 'V', 'GUG': 'V',
    'UCU': 'S', 'UCC': 'S', 'UCA': 'S', 'UCG': 'S',
    'CCU': 'P', 'CCC': 'P', 'CCA': 'P', 'CCG': 'P',
    'ACU': 'T', 'ACC': 'T', 'ACA': 'T', 'ACG': 'T',
    'GCU': 'A', 'GCC': 'A', 'GCA': 'A', 'GCG': 'A',
    'UAU': 'Y', 'UAC': 'Y', 'UAA': 'X', 'UAG': 'X',
    'CAU': 'H', 'CAC': 'H', 'CAA': 'Q', 'CAG': 'Q',
```

```
    'AAU': 'N', 'AAC': 'N', 'AAA': 'K', 'AAG': 'K',
    'GAU': 'D', 'GAC': 'D', 'GAA': 'E', 'GAG': 'E',
    'UGU': 'C', 'UGC': 'C', 'UGA': 'X', 'UGG': 'W',
    'CGU': 'R', 'CGC': 'R', 'CGA': 'R', 'CGG': 'R',
    'AGU': 'S', 'AGC': 'S', 'AGA': 'R', 'AGG': 'R',
    'GGU': 'G', 'GGC': 'G', 'GGA': 'G', 'GGG': 'G'
}

# Assign unique colors for each amino acid and stop codon
color_map = {
    'F': '#1f77b4', 'L': '#ff7f0e', 'I': '#2ca02c', 'M': '#d62728',
    'V': '#9467bd', 'S': '#8c564b', 'P': '#e377c2', 'T': '#7f7f7f',
    'A': '#bcbd22', 'Y': '#17becf', 'H': '#aec7e8', 'Q': '#ffbb78',
    'N': '#98df8a', 'K': '#ff9896', 'D': '#c5b0d5', 'E': '#c49c94',
    'C': '#f7b6d2', 'W': '#c7c7c7', 'R': '#dbdb8d', 'G': '#9edae5',
    'X': '#000000'  # Black for stop codons
}

# Coordinates conversion for nucleotide positions
nucleotide_pos = {'G': 0, 'A': 0.333, 'C': 0.667, 'U': 1.0}

# Calculate center of mass for each amino acid group
centers = {}
centers_aa = {}  # This will map centers to amino acids directly
for codon, aa in genetic_code.items():
    x, y, z = nucleotide_pos[codon[0]], nucleotide_pos[codon[1]],
nucleotide_pos[codon[2]]
    if aa not in centers:
        centers[aa] = []
    centers[aa].append(np.array([x, y, z]))
for aa in centers:
    centers[aa] = np.mean(centers[aa], axis=0)
    centers_aa[tuple(centers[aa])] = aa  # Map the mean center to its amino acid

# Convert centers to a list of points for the convex hull calculation
```

```
points = np.array([center for center in centers.values()])
hull = ConvexHull(points)

# Codon degeneracy mapping for each amino acid
degeneracy = {
    'F': 2, 'L': 6, 'I': 3, 'M': 1, 'V': 4, 'S': 6,
    'P': 4, 'T': 4, 'A': 4, 'Y': 2, 'H': 2, 'Q': 2,
    'N': 2, 'K': 2, 'D': 2, 'E': 2, 'C': 2, 'W': 1,
    'R': 6, 'G': 4, 'X': 3  # Assuming 'X' (stop codon) has 3 variations
}

# Prepare the plot
fig = plt.figure(figsize=(12, 8))
ax = fig.add_subplot(111, projection='3d')
ax.set_title('3D Convex Hull of Amino Acid Centers of Mass', color='black')

# Draw the convex hull using a Poly3DCollection
hull_faces = Poly3DCollection([points[simplex] for simplex in hull.simplices],
                              facecolors='cyan', linewidths=1, edgecolors='r', alpha=0.25)
ax.add_collection3d(hull_faces)

# Calculate and print the sum of degeneracy for each face
print("Degeneracy for each face:")
for simplex in hull.simplices:
    face_aa = [centers_aa[tuple(points[vertex])] for vertex in simplex]
    face_degeneracy = sum(degeneracy[aa] for aa in face_aa)
    print(f"Face defined by vertices {face_aa}: Total Degeneracy =
{face_degeneracy}")

# Setting axes labels
ax.set_xlabel('1st Codon Position')
ax.set_ylabel('2nd Codon Position')
ax.set_zlabel('3rd Codon Position')

# Setting the plot limits
```

```
ax.set_xlim([0, 1])
ax.set_ylim([0, 1])
ax.set_zlim([0, 1])

# Show plot
plt.show()
```